

SEQUENCE LISTING

<110> Inbe, Hisayo
Encinas, Jeffrey

<120> Regulation of Human P2Y15 G
Protein-Coupled Receptor

<130> 11582-010-999

<140> 10/529,278

<141> 2005-03-25

<150> PCT/EP2003/010666

<151> 2003-09-25

<150> 60/442,891

<151> 2003-01-28

<150> 60/413,840

<151> 2002-09-27

<160> 10

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1014

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1)...(1014)

<400> 1

atg aat gag cca cta gac tat tta gca aat gct tct gat ttc ccc gat	48
Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp	
1 5 10 15	

tat gca gct gct ttt gga aat tgc act gat gaa aac atc cca ctc aag	96
Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys	
20 25 30	

atg cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg gga ttt	144
Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe	
35 40 45	

cca ggc aat gca gta gtg ata tcc act tac att ttc aaa atg aga cct	192
Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro	
50 55 60	

tgg aag agc agc acc atc att atg ctg aac ctg gcc tgc aca gat ctg	240
Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu	
65 70 75 80	

ctg tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc agt ggc	288
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly	
85 90 95	

gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc ttc agc	336
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser	
100 105 110	

ttc cat ttc aac ctg tat agc agc atc ctc ttc ctc acc tgt ttc agc	384
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser	
115 120 125	
atc ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt tcc att	432
Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile	
130 135 140	
cac aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg atc att	480
His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile	
145 150 155 160	
tca ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca acc aac	528
Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn	
165 170 175	
agg acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat gaa ctc	576
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu	
180 185 190	
aat act att aag tgg tac aac ctg att ttg act gca act act ttc tgc	624
Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys	
195 200 205	
ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg att atc cac act	672
Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr	
210 215 220	
ctg acc cat gga ctg caa act gac agc tgc ctt aag cag aaa gca cga	720
Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg	
225 230 235 240	
agg cta acc att ctg cta ctc ctt gca ttt tac gta tgt ttt tta ccc	768
Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro	
245 250 255	
ttc cat atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc	816
Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile	
260 265 270	
agt tgt tcc att gag aat cag atc cat gaa gct tac atc gtt tct aga	864
Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg	
275 280 285	
cca tta gct gct ctg aac acc ttt ggt aac ctg tta cta tat gtg gtg	912
Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val	
290 295 300	
gtc agc gac aac ttt cag cag gct gtc tgc tca aca gtg aga tgc aaa	960
Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys	
305 310 315 320	
gta agc ggg aac ctt gag caa gca aag aaa att agt tac tca aac aac	1008
Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn	
325 330 335	
cct tga	1014
Pro *	

<210> 2
 <211> 337
 <212> PRT
 <213> Homo Sapiens

<400> 2
 Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
 1 5 10 15
 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
 20 25 30
 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
 35 40 45
 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
 50 55 60
 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
 65 70 75 80
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
 100 105 110
 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125
 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140
 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
 145 150 155 160
 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
 165 170 175
 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
 180 185 190
 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
 195 200 205
 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
 210 215 220
 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
 225 230 235 240
 Arg Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
 245 250 255
 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
 260 265 270
 Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
 275 280 285
 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 290 295 300
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
 305 310 315 320
 Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn
 325 330 335
 Pro

<210> 3
 <211> 1014
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(1014)

<400> 3
 atg att gag cca ctg gac agt cca gcc agt gat tcg gat ttc ctg gat 48
 Met Ile Glu Pro Leu Asp Ser Pro Ala Ser Asp Ser Asp Phe Leu Asp
 1 5 10 15

tac cca agt gct ctg gga aac tgc acc gac gag caa atc tca ttc aag	96
Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys	
20 25 30	
atg cag tac ctt ccc gtc atc tat agc atc atc ttc ctc gtg ggc ttc	144
Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe	
35 40 45	
ccg ggg aac aca gtg gcc atc tcc atc tac att ttc aag atg cgg ccg	192
Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro	
50 55 60	
tgg agg ggc agt aca gtc atc atg ctg aac ctg gcc ttg acg gac ttg	240
Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu	
65 70 75 80	
ctg tat ctg acc agc ctc ccg ttc ctc atc cat tac tat gcc agt ggt	288
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly	
85 90 95	
gaa aac tgg atc ttt gga gat ttc atg tgc aag ttc atc cgc ttc ggc	336
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly	
100 105 110	
ttc cac ttc aac ctc tac agc agc att ctc ttc ctc acc tgc ttc agt	384
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser	
115 120 125	
ctc ttc cgt tac gtt gtg atc att cac ccg atg agc tgc ttt tct att	432
Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile	
130 135 140	
cag aaa act cgc tgg gca gtg gta gct tgt gcc ggg gtg tgg gtc att	480
Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile	
145 150 155 160	
tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc	528
Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr	
165 170 175	
cgg acc aat agg tct gct tgc ctt gac ctc acc agt tca gat gac ctc	576
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu	
180 185 190	
act act atc aag tgg tac aat ctc att ttg aca gcc acc act ttc tgc	624
Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys	
195 200 205	
ctg cca ttg gtg ata gtg aca ctt tgc tac acg aca att atc agt acc	672
Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr	
210 215 220	
ctg act cac ggg cct cgg acc cac agc tgc ttt aag cag aag gct cgg	720
Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg	
225 230 235 240	
aga ctg act att ctg ctc ctc ctt gtt ttc tat ata tgt ttc tta ccc	768
Arg Leu Thr Ile Leu Leu Leu Leu Val Phe Tyr Ile Cys Phe Leu Pro	
245 250 255	
ttc cac atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc	816
Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile	
260 265 270	

agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtt tct aga	864
Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg	
275 280 285	
cca tta gct gct ctc aac acc ttt ggc aac ctg ctg tta tat gtt gtg	912
Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val	
290 295 300	
gtc agc aat aac ttc cag cag gca ttc tgc tct ata gtg aga tgc aaa	960
Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys	
305 310 315 320	
gcc agt ggg gac ctt gaa caa gga aag aaa gac agt tgc tca aac aac	1008
Ala Ser Gly Asp Leu Glu Gln Gly Lys Lys Asp Ser Cys Ser Asn Asn	
325 330 335	
cct tga	1014
Pro *	

<210> 4
 <211> 337
 <212> PRT
 <213> Mus musculus

<400> 4

Met	Ile	Glu	Pro	Leu	Asp	Ser	Pro	Ala	Ser	Asp	Ser	Asp	Phe	Leu	Asp
1				5					10					15	
Tyr	Pro	Ser	Ala	Leu	Gly	Asn	Cys	Thr	Asp	Glu	Gln	Ile	Ser	Phe	Lys
			20					25					30		
Met	Gln	Tyr	Leu	Pro	Val	Ile	Tyr	Ser	Ile	Ile	Phe	Leu	Val	Gly	Phe
		35					40					45			
Pro	Gly	Asn	Thr	Val	Ala	Ile	Ser	Ile	Tyr	Ile	Phe	Lys	Met	Arg	Pro
	50					55					60				
Trp	Arg	Gly	Ser	Thr	Val	Ile	Met	Leu	Asn	Leu	Ala	Leu	Thr	Asp	Leu
65					70					75					80
Leu	Tyr	Leu	Thr	Ser	Leu	Pro	Phe	Leu	Ile	His	Tyr	Tyr	Ala	Ser	Gly
				85					90					95	
Glu	Asn	Trp	Ile	Phe	Gly	Asp	Phe	Met	Cys	Lys	Phe	Ile	Arg	Phe	Gly
			100					105					110		
Phe	His	Phe	Asn	Leu	Tyr	Ser	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Phe	Ser
		115					120					125			
Leu	Phe	Arg	Tyr	Val	Val	Ile	Ile	His	Pro	Met	Ser	Cys	Phe	Ser	Ile
	130					135					140				
Gln	Lys	Thr	Arg	Trp	Ala	Val	Val	Ala	Cys	Ala	Gly	Val	Trp	Val	Ile
145					150					155					160
Ser	Leu	Val	Ala	Val	Met	Pro	Met	Thr	Phe	Leu	Ile	Thr	Ser	Thr	Thr
				165					170						175
Arg	Thr	Asn	Arg	Ser	Ala	Cys	Leu	Asp	Leu	Thr	Ser	Ser	Asp	Asp	Leu
		180						185					190		
Thr	Thr	Ile	Lys	Trp	Tyr	Asn	Leu	Ile	Leu	Thr	Ala	Thr	Thr	Phe	Cys
		195					200					205			
Leu	Pro	Leu	Val	Ile	Val	Thr	Leu	Cys	Tyr	Thr	Thr	Ile	Ile	Ser	Thr
	210					215					220				
Leu	Thr	His	Gly	Pro	Arg	Thr	His	Ser	Cys	Phe	Lys	Gln	Lys	Ala	Arg
225					230					235					240
Arg	Leu	Thr	Ile	Leu	Leu	Leu	Leu	Val	Phe	Tyr	Ile	Cys	Phe	Leu	Pro
				245					250					255	
Phe	His	Ile	Leu	Arg	Val	Ile	Arg	Ile	Glu	Ser	Arg	Leu	Leu	Ser	Ile
		260					265					270			
Ser	Cys	Ser	Ile	Glu	Ser	His	Ile	His	Glu	Ala	Tyr	Ile	Val	Ser	Arg
		275					280					285			

Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 290 295 300
 Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys
 305 310 315 320
 Ala Ser Gly Asp Leu Glu Gln Gly Lys Lys Asp Ser Cys Ser Asn Asn
 325 330 335
 Pro

<210> 5
 <211> 1014
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)...(1014)

<400> 5
 atg att gag aca ctg gac agc cca gcc aat gat tct gat ttc ctg gat 48
 Met Ile Glu Thr Leu Asp Ser Pro Ala Asn Asp Ser Asp Phe Leu Asp
 1 5 10 15
 tac ata act gct ttg gaa aac tgc act gat gag caa atc tca ttc aag 96
 Tyr Ile Thr Ala Leu Glu Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
 20 25 30
 atg cag tac ctt ccc gtc atc tac agc atc atc ttt ctc gtg ggc ttc 144
 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45
 ccg gga aat acg gtg gcg att tcc atc tac gtt ttc aag atg cga cct 192
 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Val Phe Lys Met Arg Pro
 50 55 60
 tgg aag agc agt acc atc atc atg ctg aac ctg gcc ttg acg gac ttg 240
 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80
 ctg tat ctg acc agc ctc cct ttc ctc atc cat tat tac gcg agc ggt 288
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 gaa aac tgg atc ttc ggg gat ttc atg tgc aag ttc atc cga ttt ggc 336
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
 100 105 110
 ttc cat ttc aac ctt tac agc agc atc ctc ttc ctc acc tgc ttt agc 384
 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
 115 120 125
 ctc ttc cgt tac att gtg atc att cac ccg atg agc tgt ttt tct att 432
 Leu Phe Arg Tyr Ile Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
 130 135 140
 cag aag act cga tgg gcg gtg gtg gct tgt gct ggg gtg tgg gtc att 480
 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
 145 150 155 160
 tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc 528
 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
 165 170 175

cgg acc aat agg tct gct tgc ctt gac ctc acc agc tca gat gac ctc	576
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu	
180 185 190	
act act atc aaa tgg tac aat ctc att ttg acg gct acc act ttc tgc	624
Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys	
195 200 205	
ctg ccc ttg ctg ata gtg aca ctc tgc tac acg acg att atc agc acc	672
Leu Pro Leu Leu Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr	
210 215 220	
ctg act cac gga cct cgg acc cac agc tgc ttt aag cag aag gct cgg	720
Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg	
225 230 235 240	
agg ctg acg atc ctg ctc ctc ctt gtg ttc tat gta tgc ttt tta ccc	768
Arg Leu Thr Ile Leu Leu Leu Leu Val Phe Tyr Val Cys Phe Leu Pro	
245 250 255	
ttc cac atc ctt agg gtc att cgg atc gaa tct cgc ctg ctt tca atc	816
Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile	
260 265 270	
agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtc tct agg	864
Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg	
275 280 285	
cca tta gct gcc ctc aac acc ttt ggc aac ctg ctg tta tat gtc gtc	912
Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val	
290 295 300	
gtc agc aat aac ttc cag cag gca ttc tgc tcc gca gtg aga tgt aaa	960
Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ala Val Arg Cys Lys	
305 310 315 320	
gcc atc ggg gac ctt gaa caa gca aag aaa gac agt tgc tca aac aac	1008
Ala Ile Gly Asp Leu Glu Gln Ala Lys Lys Asp Ser Cys Ser Asn Asn	
325 330 335	
ccc tga	1014
Pro *	

<210> 6
 <211> 337
 <212> PRT
 <213> Rattus norvegicus

<400> 6
 Met Ile Glu Thr Leu Asp Ser Pro Ala Asn Asp Ser Asp Phe Leu Asp
 1 5 10 15
 Tyr Ile Thr Ala Leu Glu Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
 20 25 30
 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
 35 40 45
 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Val Phe Lys Met Arg Pro
 50 55 60
 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
 65 70 75 80
 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 85 90 95
 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly

<210> 9
<211> 28
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (1)...(28)

<400> 9
gccaaactga actctcttgt tttcttgc

28

<210> 10
<211> 24
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (1)...(24)

<400> 10
gccctggctt tggcacatga ttac

24